```
FHF-1          ----------MAAAIASSLIRQKRQARESNS-DRVSASKRRSSPSKDG-R 38
FGF-10         --------------------------------------------------
FHF-4          ----------MAAAIASGLIRQKRQAREQHW-DRPSASRRRSSPSKN--R 37
FHF-2          ----------MAAAIASSLIRQKRQARER---EKSNACKCVSSPSKG--K 35
FHF-3          -----------MAALASSLIRQKREVREPGG-SRPVSAQRRVCP-RGT-K 36
FGF4_HUMAN     ----------MS-GPGTAAVALLPAVLLALL-APWAGRGGAAAPTAPN-G 37
FGF6_HUMAN     MALGQKLFITMSRGAGRLQGTLWALVFLGIL-VGMVVP--SPAGTRAN-N 46
FGF2_HUMAN     --------------------------------------------------
FGF1_HUMAN     --------------------------------------------------
KGF-2          ----------MWKWILTHCASAFPHLPGCCC-CCFLLLFLVSSVPVTC-Q 38
FGF7_HUMAN     ----------MHKWILTWILPTLLYR-S-----CFHIICLVGTISLAC-N 33
ZGI_HUZFGF     ----------MY-SAPSACTCLCLHFLLLCF-QVQ-------VLVAEE-N 30
FGF8_HUMAN     ----------MG-SPRSALSCLLLHLLVLCL-QAQEGPGRGPALGREL-A 37
FGF5_HUMAN     ----------MSLSFLLLLFFSHLILSAWAHGEKRLAPKGQPGPAATDRN 40
FGF9_HUMAN     ------------MAPLGEVGNYFGVQDAVPFGNVPVLP--VDSPVLLS-D 35
FGF3_HUMAN     ---------------MGLIWLLLLSLLEP-------G-----WPAAGPGA 23

FHF-1          SLCERHV---LGVFSKVRFCSGR----------KRPVRRRPEPQLKGIVT 75
FGF-10         -------------------------------------MASKEPQLKGIVT 13
FHF-4          GLCNGNL---VDIFSKVRIFGLK----------KRRLRRQ-DPQLKGIVT 73
FHF-2          TSCDKNK---LNVFSRVKLFGSK----------KRRRRRP-EPQLKGIVT 71
FHF-3          SLCQKQL---LILLSKVRLCGGRP---------ARPDRGP-EPQLKGIVT 73
FGF4_HUMAN     TLEAELERR-WESLVALSLARLPVAAQPKE-AAVQSGAGDYLLG-IKRLR 84
FGF6_HUMAN     TLLDS--RG-WGTLLSRSRAGL---AG--E-IAGVNWESGYLVG-IKRQR 86
FGF2_HUMAN     ----------MAAGSITTLPALPE----------DGGSGAFPPGHFKDPK 30
FGF1_HUMAN     ----------MAEGEITTFTALTE----------KFN---LPPGNYKKPK 27
KGF-2          ALGQDMVSP-EATNSSSSSFSSPSSAG------RHVRSYNHLQG-DVRWR 80
FGF7_HUMAN     DMTPEQM----ATNVNCS---SPE---------RHTRSYDYMEGGDIRVR 67
ZGI_HUZFGF     VDFRID-------------VEK------------QTRARDDVSRKQLRLY 55
FGF8_HUMAN     SLFRAGR---EPQGVSQQHVRE------------QSLVTDQLSRRLIRTY 72
FGF5_HUMAN     PIGSSSRQSSSSAMSSSSASSSPAASLGSQGSGLEQSSFQWSPS-GRRTG 89
FGF9_HUMAN     HLGQS-------E--AGGLPRGP-----------AVTDLDHLKG-ILRRR 64
FGF3_HUMAN     RLRRD--------------AGG------------RGGVYEHLGG-APRRR 46

FHF-1          RLFSQQ--GYFLQMHPDGTIDGTKDENSDYTLFNLIPVGLR-VVAIQGVK 122
FGF-10         RLFSQQ--GYFLQMHPDGTIDGTKDENSDYTLFNLIPVGLR-VVAIQGVK 60
FHF-4          RLYCRQ--GYYLQMHPDGALDGTKDDSTNSTLFNLIPVGLR-VVAIQGVK 120
FHF-2          KLYSRQ--GYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLR-VVAIQGVQ 118
FHF-3          KLFCRQ--GFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLR-VVTIQSAK 120
FGF4_HUMAN     RLYCNVGIGFHLQALPDGRIGGAHADT-RDSLLELSPVERG-VVSIFGVA 132
FGF6_HUMAN     RLYCNVGIGFHLQVLPDGRISGTHEEN-PYSLLEISTVERG-VVSLFGVR 134
FGF2_HUMAN     RLYCKNG-GFFLRIHPDGRVDGVREKSDPHIKLQLQAEERG-VVSIKGVC 78
FGF1_HUMAN     LLYCSNG-GHFLRILPDGTVDGTRDRSDQHIQLQLSAESVG-EVYIKSTE 75
KGF-2          KLFSFT--KYFLKIEKNGKVSGTKKENCPYSILEITSVEIG-VVAVKAIN 127
FGF7_HUMAN     RLFCRT--QWYLRIDKRGKVKGTQEMKNNYNIMEIRTVAVG-IVAIKGVE 114
ZGI_HUZFGF     QLYSRTS-GKHIQVLG-RRISARGEDGDKYAQLLVETDTFGSQVRIKGKE 103
FGF8_HUMAN     QLYSRTS-GKHVQVLANKRINAMAEDGDPFAKLIVETDTFGSRVRVRGAE 121
FGF5_HUMAN     SLYCRVGIGFHLQIYPDGKVNGSHEAN-MLSVLEIFAVSQG-IVGIRGVF 137
FGF9_HUMAN     QLYCRT--GFHLEIFPNGTIQGTRKDHSRFGILEFISIAVG-LVSIRGVD 111
FGF3_HUMAN     KLYCAT--KYHLQLHPSGRVNGSLENS-AYSILEITAVEVG-IVAIRGLF 92
                *:.      .:.      : .            : . .       * : .
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Fig. 1

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FHF-1         ASLYVAMNGEGYLYSSDV-FTPECKFKESVFENYYVIYSSTLYRQQESG- 170
FGF-10        ASLYVAMNGEGYLYSSDV-FTPECKFKESVFENYYVIYSSTLYRQQESG- 108
FHF-4         TGLYIAMNGEGYLYPSEL-FTPECKFKESVFENYYVIYSSMLYRQQESG- 168
FHF-2         TKLYLAMNSEGYLYTSEL-FTPECKFKESVFENYYVTYSSMIYRQQQSG- 166
FHF-3         LGHYMAMNAEGLLYSSPH-FTAECRFKECVFENYYVLYASALYRQRRSG- 168
FGF4_HUMAN    SRFFVAMSSKGKLYGSPF-FTDECTFKEILLPNNYNAYESYKYPG----- 176
FGF6_HUMAN    SALFVAMNSKGRLYATPS-FQEECKFRETLLPNNYNAYESDLYQG----- 178
FGF2_HUMAN    ANRYLAMKEDGRLLASKC-VTDECFFFERLESNNYNTYRSRKYTS----- 122
FGF1_HUMAN    TGQYLAMDTDGLLYGSQT-PNEECLFLERLEENHYNTYISKKHAEK--N- 121
KGF-2         SNYYLAMNKKGKLYGSKE-FNNDCKLKERIEENGYNTYASFNWQHN--G- 173
FGF7_HUMAN    SEFYLAMNKEGKLYAKKE-CNEDCNFKELILENHYNTYASAKWTHN--G- 160
ZGI_HUZFGF    TEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYSG----- 148
FGF8_HUMAN    TGLYICMNKKGKLIAKSNGKGKDCVFTEIVLENNYTALQNAKYEG----- 166
FGF5_HUMAN    SNKFLAMSKKGKLHASAK-FTDDCKFRERFQENSYNTYASAIHRTEKTG- 185
FGF9_HUMAN    SGLYLGMNEKGELYGSEK-LTQECVFREQFEENWYNTYSSNLYKHVDTG- 159
FGF3_HUMAN    SGRYLAMNKRGRLYASEH-YSAECEFVERIHELGYNTYASRLYRTVSSTP 141
                :: *.  * *  .     :* : * .   *    .

FHF-1         ---------RAWFLGLNKEGQIMKG--NRVKKTKPSSHFVPKPIEVCMYR 209
FGF-10        ---------RAWFLGLNKEGQIMKG--NRVEKTKPSSHFVPKPIEVCMYR 147
FHF-4         ---------RAWFLGLNKEGQAMKG--NRVKKTKPAAHFLPKPLEVAMYR 207
FHF-2         ---------RGWYLGLNKEGEIMKG--NHVKKNKPAAHFLPKPLKVAMYK 205
FHF-3         ---------RAWYLGLDKEGQVMKG--NRVKKTKAAAHFLPKLLEVAMYQ 207
FGF4_HUMAN    -----------MFIALSKNGKTKKG--NRVSPTMKVTHFLPRL------- 206
FGF6_HUMAN    -----------TYIALSKYGRVKRG--SKVSPIMTVTHFLPRI------- 208
FGF2_HUMAN    -----------WYVALKRTGQYKLG--SKTGPGQKAILFLPMSAKS---- 155
FGF1_HUMAN    -----------WFVGLKKNGSCKRG--PRTHYGQKAILFLPLPVSSD--- 155
KGF-2         ---------RQMYVALNGKGAPRRG--QKTRRKNTSAHFLPMVVHS---- 208
FGF7_HUMAN    ---------GEMFVALNQKGIPVRG--KKTKKEQKTAHFLPMAIT----- 194
ZGI_HUZFGF    -----------WYVGFTKKGRPRKG--PKTRENQQDVHFMKRYPKGQPEL 185
FGF8_HUMAN    -----------WYMAFTRKGRPRKG--SKTRQHQREVHFMKRLPRGHHTT 203
FGF5_HUMAN    ---------REWYVALNKRGKAKRGCSPRVKPQHISTHFLPRFKQSEQ-P 225
FGF9_HUMAN    ---------RRYYVALNKDGTPREG--TRTKRHQKFTHFLPRPVDPDKVP 198
FGF3_HUMAN    GARRQPSAERLWYVSVNGKGRPRRG--FKTRRTQKSSLFLPRVLDHRDHE 189
                         ::..   *    *   :.        *:

FHF-1         EPSLHEIGEKQ----GRS--RKSSGTPTMNGGKVVNQDST---------- 243
FGF-10        EPSLHEIGENK----GVQ--GKFWTPP----------------------- 168
FHF-4         EPSLHDVGETVPKP-GVTPSKSTSASAIMNGGKPVNKSKTT--------- 247
FHF-2         EPSLHDLTEFSRSG-SGTPTKSRSVSGVLNGGKSMSHNEST--------- 245
FHF-3         EPSLHSVPEAS-------P--SSPPAP----------------------- 225
FGF4_HUMAN    --------------------------------------------------
FGF6_HUMAN    --------------------------------------------------
FGF2_HUMAN    --------------------------------------------------
FGF1_HUMAN    --------------------------------------------------
KGF-2         --------------------------------------------------
FGF7_HUMAN    --------------------------------------------------
ZGI_HUZFGF    QKPFKYTTVTK-----RSRR--IRPTHPA--------------------- 207
FGF8_HUMAN    EQSLRFEFLNYPPF-TRSLRGSQRTWAPEPR------------------- 233
FGF5_HUMAN    ELSFTVTVPEKKNP-PSPIKSKIPLSAPRKNTNSVKYRLKFRFG------ 268
FGF9_HUMAN    ELYKDILSQS---------------------------------------- 208
FGF3_HUMAN    MVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH 239
```

Fig. 2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	1.00	0.39	0.43	0.29	0.46	0.33	0.36	0.38	0.37	0.41	0.39	0.40	0.42	0.40	0.35	0.38
2		1.00	0.38	0.34	0.41	0.35	0.38	0.33	0.38	0.44	0.39	0.37	0.37	0.39	0.35	0.60
3			1.00	0.31	0.42	0.34	0.33	0.36	0.34	0.38	0.35	0.37	0.41	0.46	0.35	0.35
4				1.00	0.34	0.53	0.26	0.24	0.26	0.31	0.28	0.30	0.30	0.31	0.28	0.32
5					1.00	0.35	0.39	0.43	0.39	0.39	0.43	0.42	0.44	0.43	0.40	0.43
6						1.00	0.33	0.31	0.33	0.31	0.32	0.34	0.34	0.32	0.36	0.36
7							1.00	0.34	0.98	0.33	0.76	0.81	0.34	0.37	0.67	0.42
8								1.00	0.34	0.54	0.34	0.37	0.36	0.36	0.34	0.38
9									1.00	0.33	0.66	0.72	0.34	0.37	0.62	0.42
10										1.00	0.32	0.35	0.40	0.37	0.32	0.43
11											1.00	0.68	0.36	0.38	0.58	0.41
12												1.00	0.36	0.33	0.62	0.42
13													1.00	0.47	0.34	0.32
14														1.00	0.30	0.31
15															1.00	0.38
16																1.00

Fig. 3